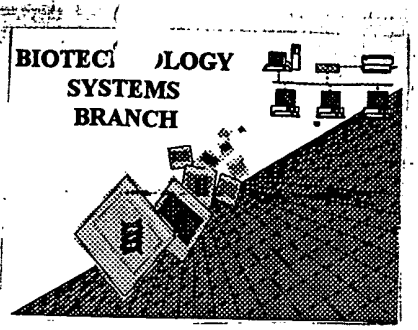
A. Wibelik

RAW SEQUENCE LISTING ERROR REPORT



RECEIVED

OCT 19 2000

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/271,584

Source: 1638

Date Processed by STIC: 10-3-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

[redacted]aw Sequence Listing Error [redacted]ummary

ERROR DETECTED	SUGGESTED CORRECTION

SERIAL NUMBER: 09/271,584

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

1638

RAW SEQUENCE LISTING DATE: 10/03/2000
PATENT APPLICATION: US/09/271,584 TIME: 16:25:14

Input Set : A:\salt seq listing.txt
Output Set: N:\CRF3\10032000\I271584.raw

```
      4 <110> APPLICANT: BLUMWALD, Eduardo
      5       APSE, Maris
      6       SNEDDEN, Wayne
      7       AHARON, Gilad
      9 <120> TITLE OF INVENTION: GENETIC ENGINEERING SALT TOLERANCE IN CROP PLANTS
     11 <130> FILE REFERENCE: 1110/0039
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/271,584
     14 <141> CURRENT FILING DATE: 1999-03-18
     16 <150> PRIOR APPLICATION NUMBER: US 60/078,474
     17 <151> PRIOR FILING DATE: 1998-04-01
     19 <150> PRIOR APPLICATION NUMBER: US 60/116,111
     20 <151> PRIOR FILING DATE: 1999-01-15
     22 <160> NUMBER OF SEQ ID NOS: 37
     24 <170> SOFTWARE: PatentIn Ver. 2.1, Word 97
```

Does Not Comply
Corrected Diskette Needed

see pp. 1, 2

ERRORED SEQUENCES

```
   2247 <210> SEQ ID NO: 37
   2248 <211> LENGTH: 30
   2249 <212> TYPE: DNA
   2250 <213> ORGANISM: Synthetic
   2252 <220> FEATURE:
   2253 <223> OTHER INFORMATION: Page 55 - Primer
   2255 <400> SEQUENCE: 37
   2257 cgcgtcgaca tgttggattc tctagtgtcg                              30
E--> 2258 1
E--> 2262 37/37
```

Extraneous material at end of file must be deleted. It is causing an invalid base count error.

<210> 23
<211> 378
<212> DNA
<213> Oryza sativa

<220>
<223> Figure 8(c)

Missing mandatory <220> to <223> features to explain "n's" in the sequence. See # 10 on Error Summary Sheet.

<400> 23

caagaagcta tacattggaa ggcattctac tgaccgtgag gttgccctta tgatgctcat 60
ggcttacctt tcatatatgc tggctgagtt gctagatttg agcggcattc tcaccgtatt 120
cttctgtggt attgtaatgt cacattacac ttggcataac gtcacagaga gttcaagagt 180
tacaacaaag cacgcatttg caactctgtc cttcattgct gagacttttc tcttcctgta 240
tgttgggatg gatgcattgg atattgaaaa atgggagntt nccagtgaca gacctggnaa 300
atccattngg gtaagctcaa ttttgctagg gattggttcc tgattggaag ngctgctttt 360
gnaattcccc tggtggtc 378

This error is also indicated in sequences 24, 25, 26, 27, and 28.

Please check the listing and correct.

VERIFICATION SUMMARY DATE: 10/03/2000
PATENT APPLICATION: US/09/271,584 TIME: 16:25:15

Input Set : A:\salt seq listing.txt
Output Set: N:\CRF3\10032000\I271584.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:1698 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1698 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1698 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:23
L:1699 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1699 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
M:340 Repeated in SeqNo=23
L:1700 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:23
L:1700 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23
L:1714 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1714 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1714 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
L:1716 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1716 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
M:340 Repeated in SeqNo=24
L:1717 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:1717 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:1730 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1730 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1730 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1731 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1731 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
M:340 Repeated in SeqNo=25
L:1735 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1735 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1758 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1758 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1758 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:1775 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:1775 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1775 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
L:1794 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:1794 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:1794 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:1795 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:1795 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
M:340 Repeated in SeqNo=28
L:1796 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:1796 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:1797 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:1797 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:2258 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:37
M:254 Repeated in SeqNo=37
L:2262 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:2262 M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:31 SEQ:37